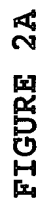




FIGURE 1A

SEQ ID NO:04	** * * ***** *	** * * * * * * * *	MATTSATTAATAA-----ATTAKPRGSSSALCQRVAGGRR-----RSGVVRCDAAAG
SEQ ID NO:12			MAVSTTFSGAKLEALLIKCSSSSSSPPPSRSS--FTTFPGQNRRTLIQ--RGVIRCDAAQP
SEQ ID NO:29			MAVSTSPFGAKLEALLIKCGSSNAATATATTTTHLSCFC-KTRKTLVQSQRGPIRCEASS
			1 60
SEQ ID NO:04	* * * * *	* * * * *	V-EAQQAQAVAKAASVAALQFKISA-DRYMKERSTIAVIGLSVHTAPVEMREKLAVAEEL
SEQ ID NO:12			-SDASSVAPNNATASALEQLKTSAADRYTKERSIIAIGLSVHTAPVEMREKLAIPEAE
SEQ ID NO:29			ASDVVADATKKAASVSALEQLKTSAADRYTKERSVVMVIGLSVHSTPVMREKLAIPEAE
			61 120
SEQ ID NO:04	*****	*****	WPRAIQELTSLNHIIEAAVLSTCNRMEIYVVALSWNRGIREVVDWMSKKSGIPASELREH
SEQ ID NO:12			WPRAIAELCSLNHIIEAAVLSTCNRMEIYVLALSQHRGVKEVMEWMSKTSSVPVSELSQH
SEQ ID NO:29			WPRAIAELCSLNHIIEAAVLSTCNRMEIYVVALSKHRGVKEVTEWMSKTSGIPVADLCQH
			121 180
SEQ ID NO:04	* * * * *	* * * * *	LFILRSSDATRHLFEVSAGLDSLVLGEGQILAQVKQVVRSGQNSGGLGKNIDRMFKDAIT
SEQ ID NO:12			RFLLYNNDATQHLFEVSAGLDSLVLGEGQILSQVKQVVKVGQGVNGFGRNISGLFKHAIT
SEQ ID NO:29			QFLLYNKDATQHLFEVSAGLDSLVLGEGQILAQVKQVVKVGQGVNGFGRNISGLFKHAIT
			181 240
SEQ ID NO:04	*****	*****	AGKRVRETNISSGAVSVSSAAVELALMKLPKSEALSARMLLIAGKMGKLVIKHLVAKG
SEQ ID NO:12			VGKRVRTETNIIASGAVSVSSAAVELAYMKLPEASHDNARMLVIGAGKMGKLVIKHLVAKG
SEQ ID NO:29			VGKRVRTETNIIAGAVSVSSAAVELALMKLPEASHANARMLVIGAGKMGKLVIKHLVAKG
			241 300



SEQ ID NO: 26	GGAQEYFGITPDVSTLGGKII GXGLPVGAYGGRKD IMEMVAPAGPMYQAGTLSGNPLAMTA *****
SEQ ID NO: 30	GGAQEYFGITPDVTTLGGKII GGGLPVGAYGGRKD IMEMVAPAGPMYQAGTLSGNPLAMTA 301 360

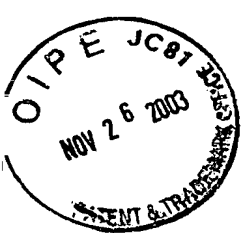


FIGURE 2B

GIHTLKRLEPETYDYLDKITGDLVRGVLDAGAKTGHEMCGGHIRGMFGFFFTAGP VHNF
GIHTLKRLEPETYDYLDKVTGELVRGILDVGAKTGHEMCGGHIRGMFGFFFTAGP VHNF
361 420

GDAKKSDTAKFGRFYRGMLEEGVYLAPSQFEAGFTSLAHTSQDIEKTVEAAAKVLRRI
DDAKKSDTAKFGRFHRGMLGEGVYLAPSQFEAGFTSLAHTTQDIEKTVEAAAEKVLRWI
421 478

SEQ ID NO:26
SEQ ID NO:30

SEQ ID NO:26
SEQ ID NO:30